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PAGE: 1

**RAW SEQUENCE LISTING
PATENT APPLICATION US/09/442,143**

DATE: 03/08/2000
TIME: 04:40:44

INPUT SET: S34972.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

412

SEQUENCE LISTING

(1) General Information:

ENTERED

(i) APPLICANT: Levy, Gary
Clark, David A.

(ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation

(iii) NUMBER OF SEQUENCES: 4

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: BERESKIN & PARR
- (B) STREET: 40 King Street West
- (C) CITY: Toronto
- (D) STATE: Ontario
- (E) COUNTRY: Canada
- (F) ZIP: M5H 3Y3

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0. Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/442,143
(B) FILING DATE: 15-NOV-1999
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Gravelle, Micheline
- (B) REGISTRATION NUMBER: 40,261
- (C) REFERENCE/DOCKET NUMBER: 9579-014

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (416) .364-7311
(B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4630 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

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PATENT APPLICATION US/09/442,143DATE: 03/08/2000
TIME: 04:40:45

INPUT SET: S34972.raw

47 (D) TOPOLOGY: linear
 48 (ii) MOLECULE TYPE: other nucleic acid
 49 (vi) ORIGINAL SOURCE:
 50 (A) ORGANISM: Homo sapiens
 51 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
 52
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 56 GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG 60
 57 TAAAGAGTCT GCCAACATTT TGAGAAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT 120
 58 ACAGAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGT 180
 59 TTAAGTAATA CAATAAAAACA TTTAGATTT TGCCCAGTGC AGTCATTTG AAATTATTT 240
 60 TAAAGCAAAA AAACCCCTTT TAAACAAGAA ATCTTATGAG ATGTCATAT GCAAAACAAA 300
 61 TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCCCTTT TCCTGCCTTC AGCCTCTGAA 360
 62 GAGAAAGTTA GAAAATATT ATCATTAATG CTACATGTTT TGAACAAGCT GATATACCAA 420
 63 GTGGCCCAGA GAGCAGGTAG AAGAACCCAGC GTGGAGACAG AAAGCAAGAG GCCCGCCTGC 480
 64 CAGGGCTACC TGCAGAAAGA AAGGGCAAAG ATGCTGTAGG CAAGAGAAGT TCAGGACAGA 540
 65 CACTGGCATA GCTCAAAGAT TCACATTTGA GCAGCTGTGG AAGATGACAG TACAATTACC 600
 66 AAAATGTCGA AGGGCAAAGG AGGCAGCTAC TGGTTTGAT GAAAGACAAT TATGTCCTTT 660
 67 TAAATGGGTC TTAGACATTT AGACATTTAT ATACACTATG CTACGGACAA AGGAATAGAA 720
 68 AGTAGCACTT TTTTCTCCAC TAGTTTCTT CTCTTTTCA AGTAGATGAA GCAAAAGTCA 780
 69 ACTGCAATAG TCAGAAAAGCT GTACTTTGTT ACACTTAGAA ACTTCTAAA GTGCTTAAGA 840
 70 TTTCACCTGA AAGTCCAACA TGAAGAAAAT ACAGGCTCCC CAATGCCCA TTCTAAGAAG 900
 71 GAAAAAGGAC CATTTCATT TTAGTAACGT TTCTGTTCTA TAGACAGTTT GGATAACTAG 960
 72 CTCTTACTTT TTATCTTTAA AAACTGTTT TCCAGTGAAG TTACGTATAA TTATTTACTT 1020
 73 CAAGCGTAGT ATACCAAATT ACTTTAGAAA TGCAAGACTT TTCTTATACT TCATAAAATA 1080
 74 CATTATGAAA GTGAATCTTG TTGGCTGTGT ACATTTGACT ATAATAATTT CAATGCATAT 1140
 75 TATTTCTATT GAGAGTAAGT TACAGTTTTT GGCAAACTGC GTTGATGAG GGCTATCTCC 1200
 76 TCTTCCTGTG CGTTTCTAAA ACTTGTGATG CAAACGCTCC CACCCCTTCC TGGGAACACA 1260
 77 GAAAGCCTGA CTCAGGCCAT GGCGCTATT AAAGCAGCTC CAGCCCTGCG CACTCCCTGCG
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PATENT APPLICATION US/09/442,143DATE: 03/08/2000
TIME: 04:40:45

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100	TGGGGTGAGC AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT	1380
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112	ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGGTTGGT GATAACAGAG TTAGAGAATT	1740
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118	TGACAGCAAA GTGGCAAATC TAACATTGT TGTCAATAGT TTGGATGGCA AATGTTCAAA	1920
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120	GTGTCCCAGC CAAGAACAAA TACAGTCACG TCCAGGTATG TATAATAATG TTTTCTTATC	1980
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122	ATATGTTCAT AAATGTTATA CAGTCAGAGA TGTATCTAAA AGATTAACCT GAGTCAGTAA	2040
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124	GTTAAATAGA TGACAGATTA AGTCTTTAT TTATCAAGGT GCACAGGAAA AAATAAATAT	2100
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126	CTTCTCAAAT ATGACCACAT AAATATGACC TAATTACAAA ATCATAGTTA GTTCTGTATC	2160
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150	TGGCACAGCT GGAGATGCAT TACGTTCAA CAAACATTAC AACCAACGATC TGAAGTTTT	2880
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152	CACCACTCCA GATAAAGACA ATGATCGATA TCCTTCTGGG AACTGTGGGC TGTACTACAG	2940

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PATENT APPLICATION US/09/442,143DATE: 03/08/2000
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INPUT SET: S34972.raw

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158	ACACCCCTGGT GGCTACAAGT CCTCCTTCAA AGAGGCTAAG ATGATGATCA GACCCAAGCA	3120
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160	CTTTAAGCCA TAAATCACTC TGTTCATTCC TCCAGGTATT CGTTATCTAA TAGGGCAATT	3180
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164	CTACACAGCA TTTGAAATAA AGCTGAAAAA CAATGCATT TAAAGGAGTC CTTTGTGTT	3300
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168	TTACAATTCT TTTAATTTCT ATTGAAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT	3420
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170	AAAAAATAAT TGTTGGCTGG GTGTGGTAGC TCACGCCTGT AATCCCAGCA CTTTGGAAATG	3480
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172	TCAAGGCAGG CAGATCACCT GAGGTCAAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA	3540
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174	ACGCTGTCTC TATTAATAAT ACAAAAATAA GCCGGGCATG GTGGTACATG CCTGTAATCA	3600
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176	ACGCTGTTA TTAAAAATAC AAAAATTAGC CGGGCATGGT GGACATGCCT GTAATCCTAG	3660
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178	TACTTGGGAG GCTGAGGCAG GAGAACCGCT TGAACCTGAG AGGAAGAGGT TGCAGTGAGC	3720
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182	AATAATAAAA TTTATTCACT AGGTGGATTC TACACAAAGT AATCTGTATT TGGGCCATGA	3840
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184	TTTAAGCACA TCTGAAGGTA TATCACTCTT TTCAGGCTAT AATTATTTGG GTAATCTTCA	3900
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186	TTCTGAGACA AACTTAATCT ATATCATTAA CTTTGCAACA GAACAACCCCT ACAGCATTAA	3960
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188	GGTTCCCAGA CTAAGGGAAC TAATATCTAT ATAATTAAAC TTGTTCATTT ATCATTCTAG	4020
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192	AAAGCATTCA GAAAGCAATG TAACTGTGAA GACCAGGGTT TAAAGGTAAT TCATTTATAG	4140
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196	TGCTCTGTGT GAACAATAGC TTTTAATTAA AGATTGCTCA CTACTGTACT AGACTACTGG	4260
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202	CATAGAAGGC TAAGTTCTC TAGGACAGAT AGAAAACATG AATTTGAAA TATATAGAAC	4440
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204	AGTAGTTAAA ATACTATATA TTTCAACCCCT GGCTGGTAGA TTGCTTATTT TACTATCAGA	4500
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206 AACTAAAAGA TAGATTTTA CCCAACAGA AGTATCTGTA ATTTTATAA TTCATCAATT 4560
207
208 CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTTAAATG TGTTTAATT CATCATCGTA 4620
209
210 AAAAGGGATC 4630
211
212 (2) INFORMATION FOR SEQ ID NO:2:
213
214 (i) SEQUENCE CHARACTERISTICS:
215 (A) LENGTH: 439 amino acids
216 (B) TYPE: amino acid
217 (C) STRANDEDNESS: single
218 (D) TOPOLOGY: linear
219
220 (ii) MOLECULE TYPE: peptide
221
222
223 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
224
225 Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr
226 1 5 10 15
227
228 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp
229 20 25 30
230
231 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys
232 35 40 45
233
234 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu
235 50 55 60
236
237 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys
238 65 70 75 80
239
240 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys
241 85 90 95
242
243 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn
244 100 105 110
245
246 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn
247 115 120 125
248
249 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu
250 130 135 140
251
252 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys
253 145 150 155 160
254
255 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys
256 165 170 175
257
258 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser

PAGE: 1

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PATENT APPLICATION US/09/442,143

DATE: 03/08/2000
TIME: 04:40:46

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